

Juliette's Notebooks

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1 Data

Use data in folder dataPetkova. The rest of the data is old (Thomas.Gregor_mutant,) or from other source(eve).

DataPetkova/Data/Gap/gap_data_raw_dorsal_wt_time_series.mat is wt data for all ages.

DataPetkova/Data/Gap/gap_data_raw_dorsal_wt.mat is wt data in 38-48 min time window. Here, we have 38 embryos in 40-44 min like Petkova. Use this to create reference manifold for bayesian prediction.

Each mutant data file has mutant data and wt data. Specify genotype 2 or 1 to choose what which one you want. Mutant maps should be constructed from their own wt.

2 commonFunctions.py

1. Load gap genes. Choose if you want specific age, position, smoothness and genotype.
2. Create manifold. Linear(True) or autoencoder(False)
3. Create average map

3 trainingAutoencoder.ipynb

Train autoencoder based on WT data all positions and all ages using "gap_data_raw_dorsal_wt_time_series.mat".

4 bayesianPosterior.ipynb

- 1.(wt maps) Create bayesian posterior and plot average map for WT 40-44 min from gap_data_raw_dorsal_wt.mat.
- 2.(map at different time windows) Feed data from different time windows to WT bayesian posterior created in 1 and plot maps. (petkova fig 6)

- 3.(Probability in manifold (hidden nodes)space)Calculate prediction from bayesian posterior created earlier (for 40-44 min) for every point in hidden nodes space.
4. (Perturbative map) Move the hidden nodes by epsilon in the direction that would make the worst prediction.
- 5.(Gradient map) Calculate and plot the gradient on the prediction map and on the hidden nodes space. 6.(Map based on single hidden node) Plot x vx x^* with posterior created from a single hidden node.

5 mutantMaps.ipynb

1. Create bayesian posterior from WT data of given mutant file.
2. Feed given mutant data to WT bayesian posterior created in 1 and plot maps. (petkova fig 4)
- 3.(Reproduce directly from 4 gg) Recreate Petokva's posterior directly on gap genes data (not on hidden nodes as before) as a check.

6 evePeaks.ipynb

1. Load wt or mutant eve data and find peaks. Calculate the average positions of stripes.
- 2.Plot distributions of peaks against result of Monte Carlo.
- 3.Make animation of stripes in time.

7 monteCarlo.ipynb

- 1.Plot corners on manifold.
2. Fit force of stripes on manifold
- 3.Simulate with Monte Carlo using potential from fit.
3. Try to predict mutant (doesn't really work.)

8 makeMovie.ipynb

Creates movies of gap genes and manifold in time.

9 neuralgregnet folder

Functions created by Adrien that I use sometimes in my code. It might not be the same as the current version that Adrien uses. We tried to put everything together in the fall, but I have not kept up with his recent changes.

10 Networks folder

newWt: train on 40-44 of DataPetkova/Data/Gap/gap_data_raw_dorsal_wt.mat

newWT1: train on all(38-48 min) of DataPetkova/Data/Gap/gap_data_raw_dorsal_wt.mat

newWT2:train on all ages of DataPetkova/Data/Gap/gap_data_raw_dorsal_wt_time_series.mat

. USE THIS ONE.

11 Useful folder

Store npy files to avoid rerunning codes for maps and other arrays.

linear folder: contains maps created from linear manifold.